

RAW SEQUENCE LISTING

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Application Serial Number: 09/717,789C
Source: 1Fw16
Date Processed by STIC: 3/2/05

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IFW16

RAW SEQUENCE LISTING

DATE: 03/02/2005

PATENT APPLICATION: US/09/717,789C

TIME: 13:08:34

Input Set : A:\140140323U3.TXT

Output Set: N:\CRF4\03022005\I717789C.raw

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4 <110> APPLICANT: Chiorini, John
5     Kotin, Robert M.
6     Safer, Brian
8 <120> TITLE OF INVENTION: AAV5 VECTOR AND USES THEREOF
11 <130> FILE REFERENCE: 14014.0323U3
13 <140> CURRENT APPLICATION NUMBER: 09/717,789C
14 <141> CURRENT FILING DATE: 2000-11-21
16 <150> PRIOR APPLICATION NUMBER: PCT/US99/11958
17 <151> PRIOR FILING DATE: 1999-05-28
19 <150> PRIOR APPLICATION NUMBER: 60/087,029
20 <151> PRIOR FILING DATE: 1998-05-28
22 <160> NUMBER OF SEQ ID NOS: 26
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 4652
28 <212> TYPE: DNA
29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
32 <223> OTHER INFORMATION: Description of Artificial Sequence; Note =
33     synthetic construct
35 <400> SEQUENCE: 1
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37 caaagagctg ccagacgacg gccctctggc cgtcgcccc ccaaacgagc cagcgagcga      120
38 gcgaacgcga caggggggag agtgccacac tctcaagcaa ggggggtttg taagcagtga      180
39 tgtcataatg atgtaatgct tattgtcacg cgatagttaa tgattaacag tcatgtgatg      240
40 tgttttatcc aataggaaga aagcgcgcgt atgagttctc gcgagacttc cgggggtataa      300
41 aagaccgagt gaacgagccc gccgccattc tttgctctgg actgctagag gaccctcgct      360
42 gccatggcta ctttctatga agtcattggt cgcgtcccat ttgacgtgga ggaacatctg      420
43 cctggaattt ctgacagctt tgtggactgg gtaactggtc aaatttggga gctgcctcca      480
44 gagtcagatt taaatttgac tctggttgaa cagcctcagt tgacggtggc tgatagaatt      540
45 cgccgcgtgt tcctgtacga gtggaacaaa ttttccaagc aggagtccaa attctttgtg      600
46 cagtttgaaa agggatctga atattttcat ctgcacacgc ttgtggagac ctccggcatc      660
47 tcttccatgg tcctcgcccg ctacgtgagt cagattcgcg ccagctggt gaaagtggtc      720
48 ttccagggaa ttgaaccca gatcaacgac tgggtcgcca tcaccaaggt aaagaagggc      780
49 ggagccaata aggtggtgga ttctgggtat attccgcct acctgctgcc gaaggtccaa      840
50 ccggagcttc agtgggcgtg gacaaacctg gacgagtata aattggccgc cctgaatctg      900
51 gaggagcgca aacggctcgt cgcgcagttt ctggcagaat cctcgacgcg ctgcaggag      960
52 gcggcttcgc agcgtgagtt ctcggtgac ccggtcatca aaagcaagac ttccagaaa      1020
53 tacatggcgc tcgtcaactg gtcgtggag cacggcatca cttccgagaa gcagtggatc      1080
54 caggaaaatc aggagagcta cctctccttc aactccaccg gcaactctcg gagccagatc      1140
55 aaggccgcgc tcgacaacgc gacaaaatt atgagtctga caaaaagcgc ggtggactac      1200
56 ctcggtggga gctccgttcc cgaggacatt tcaaaaaaca gaatctggca aatttttgag      1260
57 atgaatggct acgaccggc ctacgcggga tccatcctct acggctggtg tcagcgctcc      1320

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59	gcggaggcca	tcgcccacac	tgtgcccttt	tacggctgcg	tgaactggac	caatgaaaac	1440
60	tttcccttta	atgactgtgt	ggacaaaatg	ctcatttggt	gggaggaggg	aaagatgacc	1500
61	aacaaggtgg	ttgaatccgc	caaggccatc	ctgggggggt	caaaggtgcg	ggtcgatcag	1560
62	aaatgtaaat	cctctgttca	aattgattct	acccctgtca	ttgtaacttc	caatacaaac	1620
63	atgtgtgtgg	tgggtgatgg	gaattccacg	acctttgaac	accagcagcc	gctggaggac	1680
64	cgcattgtca	aatttgaact	gactaagcgg	ctcccgccag	attttggcaa	gattactaag	1740
65	caggaagtca	aggacttttt	tgcttgggca	aaggtcaatc	aggtgccggt	gactcacgag	1800
66	tttaaagttc	ccaggaattt	ggcgggaact	aaaggggagg	agaaatctct	aaaacgcccc	1860
67	ctgggtgacg	tcaccaatac	tagctataaa	agtctggaga	agcgggcccag	gctctcattt	1920
68	gttcccgaga	cgcctcgag	ttcagacgtg	actgttgatc	ccgctcctct	gcgaccgctc	1980
69	aattggaatt	caaggtatga	ttgcaaatgt	gactatcatg	ctcaatttga	caacatttct	2040
70	aacaaatgtg	atgaatgtga	atatttgaat	cggggcaaaa	atggatgtat	ctgtcacaat	2100
71	gtaactcact	gtcaaatttg	tcatgggatt	ccccctggg	aaaaggaaaa	cttgtcagat	2160
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73	gttgatcacc	ctccagattg	gttgaagaa	gttgggtgaag	gtcttcgcga	gtttttgggc	2280
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82	ccagcctcaa	gtttgggagc	tgatacaatg	tctgcgggag	gtggcggccc	attgggagac	2820
83	aataaccaag	gtgccgatgg	agtgggcaat	gcctcgggag	attggcattg	cgattccacg	2880
84	tggatggggg	acagagtcgt	caccaagtcc	acccgaacct	gggtgctgcc	cagctacaac	2940
85	aaccaccagt	accgagagat	caaaagcggc	tccgtcgacg	gaagcaacgc	caacgcctac	3000
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88	gtcaaaatct	tcaacattca	agtcaaagag	gtcacgggtg	aggactccac	caccaccatc	3180
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91	ccgcagtacg	gttacgcgac	gctgaaccgc	gacaacacag	aaaatccac	cgagaggagc	3360
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102	acgtacaacc	tccaggaaat	cgtgcccggc	agcgtgtgga	tggagaggga	cgtgtacctc	4020
103	caaggaccca	tctgggcca	gatcccagag	acggggggcg	actttcaccc	ctctccggcc	4080
104	atgggaggat	tcggactcaa	acacccaccg	cccatgatgc	tcatcaagaa	cacgcctgtg	4140
105	cccggaaata	tcaccagctt	ctcggacgtg	cccgctcagc	gcttcatcac	ccagtacagc	4200
106	accgggcagg	tcaccgtgga	gatggagtg	gagctcaaga	aggaaaactc	caagaggtgg	4260

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107 aaccagaga tccagtacac aaacaactac aacgaccccc agtttgtgga ctttgccccg 4320
108 gacagcaccg gggaatacag aaccaccaga cctatcgga cccgatacct taccgaccc 4380
109 ctttaaccga ttcattgtgc ataccctcaa taaaccgtgt attcgtgtca gtaaaatact 4440
110 gcctcttggt gtcattcaat gaataacagc ttacaacatc tacaaaacct ccttgcttga 4500
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120 <220> FEATURE:
121 <223> OTHER INFORMATION: Description of Artificial Sequence; Note =
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124 <400> SEQUENCE: 2
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126 1 5 10 15
127 Gln Trp Ile Gln Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr
128 20 25 30
129 Gly Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys
130 35 40 45
131 Ile Met Ser Leu Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser
132 50 55 60
133 Val Pro Glu Asp Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met
134 65 70 75 80
135 Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys
136 85 90 95
137 Gln Arg Ser Phe Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala
138 100 105 110
139 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
140 115 120 125
141 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
142 130 135 140
143 Cys Val Asp Lys Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn
144 145 150 155 160
145 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
146 165 170 175
147 Val Asp Gln Lys Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val
148 180 185 190
149 Ile Val Thr Ser Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser
150 195 200 205
151 Thr Thr Phe Glu His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe
152 210 215 220
153 Glu Leu Thr Lys Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln
154 225 230 235 240
155 Glu Val Lys Asp Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val
156 245 250 255
157 Thr His Glu Phe Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala
158 260 265 270

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159 Glu Lys Ser Leu Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr
160      275      280      285
161 Lys Ser Leu Glu Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro
162      290      295      300
163 Arg Ser Ser Asp Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn
164 305      310      315      320
165 Trp Asn Ser Arg Tyr Asp Cys Lys Cys Asp Tyr His Ala Gln Phe Asp
166      325      330      335
167 Asn Ile Ser Asn Lys Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys
168      340      345      350
169 Asn Gly Cys Ile Cys His Asn Val Thr His Cys Gln Ile Cys His Gly
170      355      360      365
171 Ile Pro Pro Trp Glu Lys Glu Asn Leu Ser Asp Phe Gly Asp Phe Asp
172      370      375      380
173 Asp Ala Asn Lys Glu Gln
174 385      390
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177 <211> LENGTH: 610
178 <212> TYPE: PRT
179 <213> ORGANISM: Artificial Sequence
181 <220> FEATURE:
182 <223> OTHER INFORMATION: Description of Artificial Sequence; Note =
183     synthetic construct
185 <400> SEQUENCE: 3
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189      20      25      30
190 Gln Ile Trp Glu Leu Pro Pro Glu Ser Asp Leu Asn Leu Thr Leu Val
191      35      40      45
192 Glu Gln Pro Gln Leu Thr Val Ala Asp Arg Ile Arg Arg Val Phe Leu
193      50      55      60
194 Tyr Glu Trp Asn Lys Phe Ser Lys Gln Glu Ser Lys Phe Phe Val Gln
195 65      70      75      80
196 Phe Glu Lys Gly Ser Glu Tyr Phe His Leu His Thr Leu Val Glu Thr
197      85      90      95
198 Ser Gly Ile Ser Ser Met Val Leu Gly Arg Tyr Val Ser Gln Ile Arg
199      100     105     110
200 Ala Gln Leu Val Lys Val Val Phe Gln Gly Ile Glu Pro Gln Ile Asn
201      115     120     125
202 Asp Trp Val Ala Ile Thr Lys Val Lys Lys Gly Gly Ala Asn Lys Val
203      130     135     140
204 Val Asp Ser Gly Tyr Ile Pro Ala Tyr Leu Leu Pro Lys Val Gln Pro
205 145     150     155     160
206 Glu Leu Gln Trp Ala Trp Thr Asn Leu Asp Glu Tyr Lys Leu Ala Ala
207      165     170     175
208 Leu Asn Leu Glu Glu Arg Lys Arg Leu Val Ala Gln Phe Leu Ala Glu
209      180     185     190
210 Ser Ser Gln Arg Ser Gln Glu Ala Ala Ser Gln Arg Glu Phe Ser Ala

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211          195          200          205
212 Asp Pro Val Ile Lys Ser Lys Thr Ser Gln Lys Tyr Met Ala Leu Val
213          210          215          220
214 Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln
215 225          230          235          240
216 Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr Gly Asn Ser Arg
217          245          250          255
218 Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys Ile Met Ser Leu
219          260          265          270
220 Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser Val Pro Glu Asp
221          275          280          285
222 Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met Asn Gly Tyr Asp
223          290          295          300
224 Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys Gln Arg Ser Phe
225 305          310          315          320
226 Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala Thr Thr Gly Lys
227          325          330          335
228 Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys
229          340          345          350
230 Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys
231          355          360          365
232 Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn Lys Val Val Glu
233          370          375          380
234 Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys
235 385          390          395          400
236 Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val Ile Val Thr Ser
237          405          410          415
238 Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser Thr Thr Phe Glu
239          420          425          430
240 His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe Glu Leu Thr Lys
241          435          440          445
242 Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln Glu Val Lys Asp
243          450          455          460
244 Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val Thr His Glu Phe
245 465          470          475          480
246 Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala Glu Lys Ser Leu
247          485          490          495
248 Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr Lys Ser Leu Glu
249          500          505          510
250 Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro Arg Ser Ser Asp
251          515          520          525
252 Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn Trp Asn Ser Arg
253          530          535          540
254 Tyr Asp Cys Lys Cys Asp Tyr His Ala Gln Phe Asp Asn Ile Ser Asn
255 545          550          555          560
256 Lys Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys Asn Gly Cys Ile
257          565          570          575
258 Cys His Asn Val Thr His Cys Gln Ile Cys His Gly Ile Pro Pro Trp
259          580          585          590

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